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RAW SEQUENCE LISTING

DATE: 08/07/2002

PATENT APPLICATION: US/09/663,542

TIME: 15:51:49

Input Set : A:\PC10349AGPR Seq List.ST25.txt

Output Set: N:\CRF3\08072002\I663542.raw

#11

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3 <110> APPLICANT: Pfizer Inc.
4      Fidock, Mark D.
5      Robas, Nicola M.
7 <120> TITLE OF INVENTION: Phosphodiesterase Enzymes
9 <130> FILE REFERENCE: PC10349AGPR
11 <140> CURRENT APPLICATION NUMBER: 09/663,542
12 <141> CURRENT FILING DATE: 2000-09-15
14 <150> PRIOR APPLICATION NUMBER: US 60/177,517
15 <151> PRIOR FILING DATE: 2000-01-21
17 <150> PRIOR APPLICATION NUMBER: GB 9922124.4
18 <151> PRIOR FILING DATE: 1999-09-17
20 <160> NUMBER OF SEQ ID NOS: 16
22 <170> SOFTWARE: PatentIn version 3.1
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 684
26 <212> TYPE: PRT
27 <213> ORGANISM: Homo sapiens
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36          20          25          30
39 Ala Ser Leu Ala Glu Lys Gln Glu Lys His Gln Asp Phe Leu Ile Gln
40          35          40          45
43 Arg Gln Thr Lys Thr Lys Asp Arg Arg Phe Asn Asp Glu Ile Asp Lys
44          50          55          60
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48 65          70          75          80
51 Ser Asp Gly Glu Ile Ile Gly Val Ala Gln Ala Ile Asn Lys Ile Pro
52          85          90          95
55 Glu Gly Ala Pro Phe Thr Glu Asp Asp Glu Lys Val Met Gln Met Tyr
56          100         105         110
59 Leu Pro Phe Cys Gly Ile Ala Ile Ser Asn Ala Gln Leu Phe Ala Ala
60          115         120         125
63 Ser Arg Lys Glu Tyr Glu Arg Ser Arg Ala Leu Leu Glu Val Val Asn
64          130         135         140
67 Asp Leu Phe Glu Glu Gln Thr Asp Leu Glu Lys Ile Val Lys Lys Ile
68 145         150         155         160
71 Met His Arg Ala Gln Thr Leu Leu Lys Cys Glu Arg Cys Ser Val Leu
72          165         170         175
75 Leu Leu Glu Asp Ile Glu Ser Pro Val Val Lys Phe Thr Lys Ser Phe
76          180         185         190
79 Glu Leu Met Ser Pro Lys Cys Ser Ala Asp Ala Glu Asn Ser Phe Lys

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84          210          215          220
87 Ile Ala Glu Leu Val Ala Ser Thr Gly Leu Pro Val Asn Ile Ser Asp
88 225          230          235          240
91 Ala Tyr Gln Asp Pro Arg Phe Asp Ala Glu Ala Asp Gln Ile Ser Gly
92          245          250          255
95 Phe His Ile Arg Ser Val Leu Cys Val Pro Ile Trp Asn Ser Asn His
96          260          265          270
99 Gln Ile Ile Gly Val Ala Gln Val Leu Asn Arg Leu Asp Gly Lys Pro
100          275          280          285
103 Phe Asp Asp Ala Asp Gln Arg Leu Phe Glu Ala Phe Val Ile Phe Cys
104          290          295          300
107 Gly Leu Gly Ile Asn Asn Thr Ile Met Tyr Asp Gln Val Lys Lys Ser
108 305          310          315          320
111 Trp Ala Lys Gln Ser Val Ala Leu Asp Val Leu Ser Tyr His Ala Thr
112          325          330          335
115 Cys Ser Lys Ala Glu Val Asp Lys Phe Lys Ala Ala Asn Ile Pro Leu
116          340          345          350
119 Val Ser Glu Leu Ala Ile Asp Asp Ile His Phe Asp Asp Phe Ser Leu
120          355          360          365
123 Asp Val Asp Ala Met Ile Thr Ala Ala Leu Arg Met Phe Met Glu Leu
124          370          375          380
127 Gly Met Val Gln Lys Phe Lys Ile Asp Tyr Glu Thr Leu Cys Arg Trp
128 385          390          395          400
131 Leu Leu Thr Val Arg Lys Asn Tyr Arg Met Val Leu Tyr His Asn Trp
132          405          410          415
135 Arg His Ala Phe Asn Val Cys Gln Leu Met Phe Ala Met Leu Thr Thr
136          420          425          430
139 Ala Gly Phe Gln Asp Ile Leu Thr Glu Val Glu Ile Leu Ala Val Ile
140          435          440          445
143 Val Gly Cys Leu Cys His Asp Leu Asp His Arg Gly Thr Asn Asn Ala
144          450          455          460
147 Phe Gln Ala Lys Ser Gly Ser Ala Leu Ala Gln Leu Tyr Gly Thr Ser
148 465          470          475          480
151 Ala Thr Leu Glu His His His Phe Asn His Ala Val Met Ile Leu Gln
152          485          490          495
155 Ser Glu Gly His Asn Ile Phe Ala Asn Leu Ser Ser Lys Glu Tyr Ser
156          500          505          510
159 Asp Leu Met Gln Leu Leu Lys Gln Ser Ile Leu Ala Thr Asp Leu Thr
160          515          520          525
163 Leu Tyr Phe Glu Arg Arg Thr Glu Phe Phe Glu Leu Val Ser Lys Gly
164          530          535          540
167 Glu Tyr Asp Trp Asn Ile Lys Asn His Arg Asp Ile Phe Arg Ser Met
168 545          550          555          560
171 Leu Met Thr Ala Cys Asp Leu Gly Ala Val Thr Lys Pro Trp Glu Ile
172          565          570          575
175 Ser Arg Gln Val Ala Glu Leu Val Thr Ser Glu Phe Phe Glu Gln Gly
176          580          585          590

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179 Asp Arg Glu Arg Leu Glu Leu Lys Leu Thr Pro Ser Ala Ile Phe Asp
 180 595 600 605
 183 Arg Asn Arg Lys Asp Glu Leu Pro Arg Leu Gln Leu Glu Trp Ile Asp
 184 610 615 620
 187 Ser Ile Cys Met Pro Leu Tyr Gln Ala Leu Val Lys Val Asn Val Lys
 188 625 630 635 640
 191 Leu Lys Pro Met Leu Asp Ser Val Ala Thr Asn Arg Ser Lys Trp Glu
 192 645 650 655
 195 Glu Leu His Gln Lys Arg Leu Leu Ala Ser Thr Ala Ser Ser Ser
 196 660 665 670
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205 <212> TYPE: DNA

206 <213> ORGANISM: Homo sapiens

208 <400> SEQUENCE: 2

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213	aacaggaaaa	gcaccaggat	tttcttatac	agaggcaaac	aaaaacaaag	gatcgacgat	180
215	tcaatgatga	aatcgacaag	ctgactggat	acaagacaaa	atcattattg	tgcattgcta	240
217	tccgaagcag	tgatgggtgag	attattgggtg	tggcccaagc	gataaataag	attcctgaag	300
219	gagctccatt	tactgaagat	gatgaaaaag	ttatgcagat	gtatcttcca	ttttgtggaa	360
221	tcgccatata	taacgctcag	ctctttgctg	cctcaaggaa	agaatatgaa	agaagcagag	420
223	ctttgctaga	ggtgggttaat	gacctctttg	aagaacagac	tgacctggag	aaaattgtca	480
225	agaaaataat	gcacggggcc	caaactctgc	tgaaatgtga	gcgctgttct	gttttactcc	540
227	tagaggacat	cgaatcacca	gtggtgaaat	ttaccaaatc	ctttgaattg	atgtcccca	600
229	agtgcagtgc	tgatgctgag	aacagtttca	aagaaagcat	ggagaaatca	tcatactccg	660
231	actggcta	aaataacagc	attgctgagc	tgggtgcttc	aacaggcctt	ccagtgaaca	720
233	tcagtgatgc	ctaccaggat	ccgcgctttg	atgcagaggc	agaccagata	tctggttttc	780
235	acataagatc	tgttctttgt	gtccctat	ggaatagcaa	ccaccaaata	attggagtgg	840
237	ctcaagtgtt	aaacagactt	gatgggaaac	cttttgatga	tgcagatcaa	cgactttttg	900
239	aggctttttg	catctttttg	ggacttggca	tcaacaacac	aattatgtat	gatcaagtga	960
241	agaagtctctg	ggccaagcag	tctgttgctc	ttgatgtgct	atcataccat	gcaacatgtt	1020
243	caaaagctga	agttgacaag	tttaaggcag	ccaacatccc	tctggtgtca	gaacttgcca	1080
245	tcgatgacat	tcatttttgat	gacttttctc	tcgacgttga	tgccatgatc	acagctgctc	1140
247	tccggatgtt	catggagctg	gggatggtac	agaaatttaa	aattgactat	gagacactgt	1200
249	gtaggtggct	tttgacagtg	aggaaaaact	atcggatggt	tctataccac	aactggagac	1260
251	atgccttcaa	cgtgtgtcag	ctgatgttcg	cgatgttaac	cactgctggg	tttcaagaca	1320
253	ttctgaccga	ggtggaaatt	ttagcgggtga	ttgtgggatg	cctgtgtcat	gacctcgacc	1380
255	acaggggaac	caacaatgcc	ttccaagcta	agagtggctc	tgccctggcc	caactctatg	1440
257	gaacctctgc	taccttggag	catcaccatt	tcaaccacgc	cgtgatgatc	cttcaaagtg	1500
259	agggtcacaa	tatcttttgc	aacctgtcct	ccaaggata	tagtgacctt	atgcagcttt	1560
261	tgaagcagtc	aatattggca	acagacctca	cgctgtactt	tgagaggaga	actgaattct	1620
263	ttgaacttgt	cagtaaaggga	gaatacgatt	ggaacatcaa	aaaccatcgt	gatataattc	1680
265	gatcaatgtt	aatgacagcc	tgtgaccttg	gagccgtgac	caaaccgtgg	gagatctcca	1740
267	gacaggtggc	agaacttgta	accagtga	tcttcgaaca	aggagatcgg	gagagattag	1800
269	agctcaaaact	cactccttca	gcaatttttg	atcggaaccg	gaaggatgaa	ctgcctcggt	1860
271	tgcaactgga	gtggattgat	agcatctgca	tgcctttgta	tcaggcactg	gtgaaggtca	1920

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273 acgtgaaact gaagccgatg ctagattcag tagctacaaa cagaagtaag tgggaagagc 1980
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283 <213> ORGANISM: Homo sapiens
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288 1 5 10 15
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292 20 25 30
295 Glu Val Val Asn Asp Leu Phe Glu Glu Gln Thr Asp Leu Glu Lys Ile
296 35 40 45
299 Val Lys Lys Ile Met His Arg Ala Gln Thr Leu Leu Lys Cys Glu Arg
300 50 55 60
303 Cys Ser Val Leu Leu Leu Glu Asp Ile Glu Ser Pro Val Val Lys Phe
304 65 70 75 80
307 Thr Lys Ser Phe Glu Leu Met Ser Pro Lys Cys Ser Ala Asp Ala Glu
308 85 90 95
311 Asn Ser Phe Lys Glu Ser Met Glu Lys Ser Ser Tyr Ser Asp Trp Leu
312 100 105 110
315 Ile Asn Asn Ser Ile Ala Glu Leu Val Ala Ser Thr Gly Leu Pro Val
316 115 120 125
319 Asn Ile Ser Asp Ala Tyr Gln Asp Pro Arg Phe Asp Ala Glu Ala Asp
320 130 135 140
323 Gln Ile Ser Gly Phe His Ile Arg Ser Val Leu Cys Val Pro Ile Trp
324 145 150 155 160
327 Asn Ser Asn His Gln Ile Ile Gly Val Ala Gln Val Leu Asn Arg Leu
328 165 170 175
331 Asp Gly Lys Pro Phe Asp Asp Ala Asp Gln Arg Leu Phe Glu Ala Phe
332 180 185 190
335 Val Ile Phe Cys Gly Leu Gly Ile Asn Asn Thr Ile Met Tyr Asp Gln
336 195 200 205
339 Val Lys Lys Ser Trp Ala Lys Gln Ser Val Ala Leu Asp Val Leu Ser
340 210 215 220
343 Tyr His Ala Thr Cys Ser Lys Ala Glu Val Asp Lys Phe Lys Ala Ala
344 225 230 235 240
347 Asn Ile Pro Leu Val Ser Glu Leu Ala Ile Asp Asp Ile His Phe Asp
348 245 250 255
351 Asp Phe Ser Leu Asp Val Asp Ala Met Ile Thr Ala Ala Leu Arg Met
352 260 265 270
355 Phe Met Glu Leu Gly Met Val Gln Lys Phe Lys Ile Asp Tyr Glu Thr
356 275 280 285
359 Leu Cys Arg Trp Leu Leu Thr Val Arg Lys Asn Tyr Arg Met Val Leu
360 290 295 300
363 Tyr His Asn Trp Arg His Ala Phe Asn Val Cys Gln Leu Met Phe Ala
364 305 310 315 320
367 Met Leu Thr Thr Ala Gly Phe Gln Asp Ile Leu Thr Glu Val Glu Ile

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368          325          330          335
371 Leu Ala Val Ile Val Gly Cys Leu Cys His Asp Leu Asp His Arg Gly
372          340          345          350
375 Thr Asn Asn Ala Phe Gln Ala Lys Ser Gly Ser Ala Leu Ala Gln Leu
376          355          360          365
379 Tyr Gly Thr Ser Ala Thr Leu Glu His His His Phe Asn His Ala Val
380          370          375          380
383 Met Ile Leu Gln Ser Glu Gly His Asn Ile Phe Ala Asn Leu Ser Ser
384 385          390          395          400
387 Lys Glu Tyr Ser Asp Leu Met Gln Leu Leu Lys Gln Ser Ile Leu Ala
388          405          410          415
391 Thr Asp Leu Thr Leu Tyr Phe Glu Arg Arg Thr Glu Phe Phe Glu Leu
392          420          425          430
395 Val Ser Lys Gly Glu Tyr Asp Trp Asn Ile Lys Asn His Arg Asp Ile
396          435          440          445
399 Phe Arg Ser Met Leu Met Thr Ala Cys Asp Leu Gly Ala Val Thr Lys
400          450          455          460
403 Pro Trp Glu Ile Ser Arg Gln Val Ala Glu Leu Val Thr Ser Glu Phe
404 465          470          475          480
407 Phe Glu Gln Gly Asp Arg Glu Arg Leu Glu Leu Lys Leu Thr Pro Ser
408          485          490          495
411 Ala Ile Phe Asp Arg Asn Arg Lys Asp Glu Leu Pro Arg Leu Gln Leu
412          500          505          510
415 Glu Trp Ile Asp Ser Ile Cys Met Pro Leu Tyr Gln Ala Leu Val Lys
416          515          520          525
419 Val Asn Val Lys Leu Lys Pro Met Leu Asp Ser Val Ala Thr Asn Arg
420          530          535          540
423 Ser Lys Trp Glu Glu Leu His Gln Lys Arg Leu Leu Ala Ser Thr Ala
424 545          550          555          560
427 Ser Ser Ser Ser Pro Ala Ser Val Met Val Ala Lys Glu Asp Arg Asn
428          565          570          575

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431 <210> SEQ ID NO: 4

432 <211> LENGTH: 1925

433 <212> TYPE: DNA

434 <213> ORGANISM: Homo sapiens

436 <400> SEQUENCE: 4

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441 gctttgctag aggtggttaa tgacctcttt gaagaacaga ctgacctgga gaaaattgtc      180
443 aagaaaataa tgcacgggc ccaaaactctg ctgaaatgtg aacgctgttc tgttttactc      240
445 ctagaggaca tcgaatcacc agtggtgaaa tttaccaaat cctttgaatt gatgtcccca      300
447 aagtgcagtg ctgatgctga gaacagtttc aaagaaagca tggagaaatc atcatactcc      360
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451 atcagtgatg cctaccagga tccgcgcttt gatgcagagg cagaccagat atctggtttt      480
453 cacataagat ctgttctttg tgtccctatt tggaatagca accaccaaat aattggagtg      540
455 gctcaagtgt taaacagact tgatgggaaa ccttttgatg atgcggatca acgacttttt      600
457 gaggcttttg tcatcttttg tggacttggc atcaacaaca caattatgta tgatcaagtg      660
459 aagaagtccct gggccaagca gtctgtggct cttgatgtgc tatcatacca tgcaacatgt      720
461 tcaaaagctg aagttgacaa gtttaaggca gccaacatcc ctctggtgtc agaacttgcc      780

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/663,542

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